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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/081,301

DATE: 03/07/2002

TIME: 11:23:36

Input Set : N:\Crf3\RULE60\10081301.txt

Output Set: N:\CRF3\03072002\J081301.raw

3 <110> APPLICANT: Falco, S. Carl  
 4 Cahoon, Rebecca E.  
 5 Rafalski, J. Antoni  
 7 <120> TITLE OF INVENTION: Vitamin B Metabolism Proteins  
 9 <130> FILE REFERENCE: BB-1201  
 11 <140> CURRENT APPLICATION NUMBER: 10/081,301  
 12 <141> CURRENT FILING DATE: 2002-02-20  
 14 <150> PRIOR APPLICATION NUMBER: 09/371,056  
 15 <151> PRIOR FILING DATE: 1999-08-09  
 17 <150> PRIOR APPLICATION NUMBER: 60/096,342  
 W--> 18 <151> PRIOR FILING DATE: August 12, 1998  
 20 <160> NUMBER OF SEQ ID NOS: 16  
 22 <170> SOFTWARE: Microsoft Office 97  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 933  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Zea mays  
 29 <400> SEQUENCE: 1  
 30 atggcgcgccg cgccgatacct atccgtcgcg ctgccgtctg acaccggccg tgtgctcagc 60  
 31 atccagtccc acaccgtcca ggggtatgtt ggcaacaaat cggccgtctt tcccctgcag 120  
 32 ctcccttggt ttgatgtgga tccaataaac tctgtacagt tttctaatac tacaggatac 180  
 33 ccaacattta gaggtcaggt tcttaatggc aaacagctct gggaccttat tgaaggactg 240  
 34 gaggaataat agttgcttca ttatacccat ttattaacag gttatatagg ctcaagtttcc 300  
 35 tttttagata ctgtgtcaca agttgttgag aaattgcgat cagttaatcc tgatcttgta 360  
 36 tatgtttgtg acccagttct aggtgatgaa ggaaaactat atgttcctca ggaggtaata 420  
 37 tctgtttatc aacagaaggt tgttccagtt gcttcaatgc ttacacctaa ccaatttgaa 480  
 38 gttgaactac ttactggatt gaggatcacc tccgaagaag atgggttgac agcttgtaat 540  
 39 accctccaca gtgccggacc acagaagggtg gttataacta gtgctcttat tgaaggtaag 600  
 40 ctgctcctta tcggaagtca caaaaaaaca gaggaacaac agccagaaca atttaagatt 660  
 41 gagataccaa agatacctgc atatttcaag ggaactggag atttgacaac tgctctccta 720  
 42 ctaggatgga gtaataaata tcctgatagc ctcgagaaag cagcagaact ggcagtttcc 780  
 43 agtttgcagg cacttctgaa aagaactgtg gaagactata aaatggccgg cttcgaccca 840  
 44 tcgaccagca gcttagagat ccggttgatc caaagccagg acgagatccg aaacccaact 900  
 45 gttacatgca aggctgtgaa gtatggaagc tga 933  
 47 <210> SEQ ID NO: 2  
 48 <211> LENGTH: 310  
 49 <212> TYPE: PRT  
 50 <213> ORGANISM: Zea mays  
 52 <400> SEQUENCE: 2  
 53 Met Ala Arg Pro Pro Ile Leu Ser Val Ala Leu Pro Ser Asp Thr Gly  
 54 1 5 10 15  
 56 Arg Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn  
 57 20 25 30

ENTERED

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59 Lys Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Phe Asp Val Asp Pro
60          35          40          45
62 Ile Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Arg
63      50          55          60
65 Gly Gln Val Leu Asn Gly Lys Gln Leu Trp Asp Leu Ile Glu Gly Leu
66 65          70          75          80
68 Glu Glu Asn Gln Leu Leu His Tyr Thr His Leu Leu Thr Gly Tyr Ile
69          85          90          95
71 Gly Ser Val Ser Phe Leu Asp Thr Val Leu Gln Val Val Glu Lys Leu
72          100          105          110
74 Arg Ser Val Asn Pro Asp Leu Val Tyr Val Cys Asp Pro Val Leu Gly
75          115          120          125
77 Asp Glu Gly Lys Leu Tyr Val Pro Gln Glu Val Ile Ser Val Tyr Gln
78          130          135          140
80 Gln Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu
81 145          150          155          160
83 Val Glu Leu Leu Thr Gly Leu Arg Ile Thr Ser Glu Glu Asp Gly Leu
84          165          170          175
86 Thr Ala Cys Asn Thr Leu His Ser Ala Gly Pro Gln Lys Val Val Ile
87          180          185          190
89 Thr Ser Ala Leu Ile Glu Gly Lys Leu Leu Leu Ile Gly Ser His Lys
90          195          200          205
92 Lys Thr Glu Glu Gln Gln Pro Glu Gln Phe Lys Ile Glu Ile Pro Lys
93          210          215          220
95 Ile Pro Ala Tyr Phe Thr Gly Thr Gly Asp Leu Thr Thr Ala Leu Leu
96 225          230          235          240
98 Leu Gly Trp Ser Asn Lys Tyr Pro Asp Ser Leu Glu Lys Ala Ala Glu
99          245          250          255
101 Leu Ala Val Ser Ser Leu Gln Ala Leu Leu Lys Arg Thr Val Glu Asp
102          260          265          270
104 Tyr Lys Met Ala Gly Phe Asp Pro Ser Thr Ser Ser Leu Glu Ile Arg
105          275          280          285
107 Leu Ile Gln Ser Gln Asp Glu Ile Arg Asn Pro Thr Val Thr Cys Lys
108          290          295          300
110 Ala Val Lys Tyr Gly Ser
111 305          310
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 413
115 <212> TYPE: DNA
116 <213> ORGANISM: Oryza sativa
118 <220> FEATURE:
119 <221> NAME/KEY: unsure
120 <222> LOCATION: (380)
122 <220> FEATURE:
123 <221> NAME/KEY: unsure
124 <222> LOCATION: (384)
126 <220> FEATURE:
127 <221> NAME/KEY: unsure
128 <222> LOCATION: (388)

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Output Set: N:\CRF3\03072002\J081301.raw

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130 <220> FEATURE:
131 <221> NAME/KEY: unsure
132 <222> LOCATION: (410)
134 <400> SEQUENCE: 3
135 gtttaaacaa gaagatggct tgaaagcttg caatgcgcta catagtgctg gaccgcgaaa 60
136 ggtggtaata actagtgcac ttattgaaga taagctgctc ctcattggaa gccacaaaaa 120
137 agcaaaggaa caaccaccag aacaatttaa gattgagata cccaagatac ctgcatattt 180
138 cacgggcact ggagatttaa caactgccct tctactagga tggagtaata aataccctga 240
139 taaccttggg gagggcgctg aactggcggt atccatttgc aaggcacccc taaggagaac 300
140 tgtggaagac tataaaagac tgggtttgac cctccaacca acacctagag atccgcctgg 360
W--> 141 attcaaaacc aaggatgaan tccnaagncc caagatacat gcaagctgtg aaa 413
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 136
145 <212> TYPE: PRT
146 <213> ORGANISM: Oryza sativa
148 <220> FEATURE:
149 <221> NAME/KEY: UNSURE
150 <222> LOCATION: (127)..(128)..(129)
152 <400> SEQUENCE: 4
153 Phe Lys Gln Glu Asp Gly Leu Lys Ala Cys Asn Ala Leu His Ser Ala
154 1 5 10 15
156 Gly Pro Arg Lys Val Val Ile Thr Ser Ala Leu Ile Glu Asp Lys Leu
157 20 25 30
159 Leu Leu Ile Gly Ser His Lys Lys Ala Lys Glu Gln Pro Pro Glu Gln
160 35 40 45
162 Phe Lys Ile Glu Ile Pro Lys Ile Pro Ala Tyr Phe Thr Gly Thr Gly
163 50 55 60
165 Asp Leu Thr Thr Ala Leu Leu Gly Trp Ser Asn Lys Tyr Pro Asp
166 65 70 75 80
168 Asn Leu Gly Glu Gly Ala Glu Leu Ala Val Ser Ile Cys Lys Ala Pro
169 85 90 95
171 Leu Arg Arg Thr Val Glu Asp Tyr Lys Arg Leu Gly Leu Thr Leu Gln
172 100 105 110
W--> 174 Pro Thr Pro Arg Asp Pro Pro Gly Phe Lys Thr Lys Asp Glu Xaa Xaa
175 115 120 125
W--> 177 Xaa Pro Lys Ile His Ala Ser Cys
178 130 135
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 812
182 <212> TYPE: DNA
183 <213> ORGANISM: Glycine max
185 <220> FEATURE:
186 <221> NAME/KEY: unsure
187 <222> LOCATION: (577)
189 <220> FEATURE:
190 <221> NAME/KEY: unsure
191 <222> LOCATION: (610)
193 <220> FEATURE:
194 <221> NAME/KEY: unsure

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Input Set : N:\Crf3\RULE60\10081301.txt

Output Set: N:\CRF3\03072002\J081301.raw

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195 <222> LOCATION: (683)
197 <220> FEATURE:
198 <221> NAME/KEY: unsure
199 <222> LOCATION: (687)
201 <220> FEATURE:
202 <221> NAME/KEY: unsure
203 <222> LOCATION: (742)
205 <220> FEATURE:
206 <221> NAME/KEY: unsure
207 <222> LOCATION: (744)
209 <220> FEATURE:
210 <221> NAME/KEY: unsure
211 <222> LOCATION: (746)
213 <220> FEATURE:
214 <221> NAME/KEY: unsure
215 <222> LOCATION: (755)
217 <220> FEATURE:
218 <221> NAME/KEY: unsure
219 <222> LOCATION: (760)
221 <220> FEATURE:
222 <221> NAME/KEY: unsure
223 <222> LOCATION: (769)
225 <220> FEATURE:
226 <221> NAME/KEY: unsure
227 <222> LOCATION: (778)
229 <220> FEATURE:
230 <221> NAME/KEY: unsure
231 <222> LOCATION: (785)..(786)
233 <220> FEATURE:
234 <221> NAME/KEY: unsure
235 <222> LOCATION: (792)
237 <220> FEATURE:
238 <221> NAME/KEY: unsure
239 <222> LOCATION: (804)
241 <400> SEQUENCE: 5
242 gcacgaggag cattttccgg gcacgaaact cgaggaattc gcgcatggcg cctccaatcc 60
243 tctcgctcgc tcttccctcg aacaccggtc gagttctcag cattcaatct cacaccgttc 120
244 aggggtatgt tggtaataaa tccgctgtct tccctctgca actactggga tatgatgtcg 180
245 atccaattaa ttccgtgcag ttttcgaatc atacaggata tccgacgttt aagggtcagg 240
246 ttttgaatgg acagcaactc tgggatctaa tcgaaggcct tgaaggaaat gattttattgt 300
247 tctatactca cttgctaaca gggttatattg gttcagagtc ttttctaaac actgtattgc 360
248 aagttgtcag caaacttcgg tcaacaaacc caggtctttc gtatgtatgt gatccagtga 420
249 tgggtgatga aggaaagctt tatgttcctc aagagctagt atcagtctat cgtgagaagg 480
250 ttgttccagt agcttcaatg ttgactccca accagtttga agcagaacta ctgacaggct 540
W--> 251 ttaggattca gtctgaagga catggccggg aggctgntag gcttctccat gcagctgggc 600
W--> 252 cttcaaaggn cataattaca agtataaata tagacgggat tcttctctc attggcagtc 660
W--> 253 atccaaaaga aaagggagag ccnccngac aatttaagat tgttattcca aaaataacca 720
W--> 254 gcttatttta cgggaacggg anancncatg actgnattcn tcttggttng agcataanta 780
W--> 255 ccannacaa ancttgagaa tgcngcgga ct 812

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Input Set : N:\Crif3\RULE60\10081301.txt

Output Set: N:\CRF3\03072002\J081301.raw

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257 <210> SEQ ID NO: 6
258 <211> LENGTH: 196
259 <212> TYPE: PRT
260 <213> ORGANISM: Glycine max
262 <220> FEATURE:
263 <221> NAME/KEY: UNSURE
264 <222> LOCATION: (178)
266 <220> FEATURE:
267 <221> NAME/KEY: UNSURE
268 <222> LOCATION: (189)
270 <400> SEQUENCE: 6
271 Met Ala Pro Pro Ile Leu Ser Leu Ala Leu Pro Ser Asn Thr Gly Arg
272   1             5             10             15
274 Val Leu Ser Ile Gln Ser His Thr Val Gln Gly Tyr Val Gly Asn Lys
275             20             25             30
277 Ser Ala Val Phe Pro Leu Gln Leu Leu Gly Tyr Asp Val Asp Pro Ile
278             35             40             45
280 Asn Ser Val Gln Phe Ser Asn His Thr Gly Tyr Pro Thr Phe Lys Gly
281             50             55             60
283 Gln Val Leu Asn Gly Gln Gln Leu Trp Asp Leu Ile Glu Gly Leu Glu
284             65             70             75             80
286 Gly Asn Asp Leu Leu Phe Tyr Thr His Leu Leu Thr Gly Tyr Ile Gly
287             85             90             95
289 Ser Glu Ser Phe Leu Asn Thr Val Leu Gln Val Val Ser Lys Leu Arg
290             100            105            110
292 Ser Thr Asn Pro Gly Leu Ser Tyr Val Cys Asp Pro Val Met Gly Asp
293             115            120            125
295 Glu Gly Lys Leu Tyr Val Pro Gln Glu Leu Val Ser Val Tyr Arg Glu
296             130            135            140
298 Lys Val Val Pro Val Ala Ser Met Leu Thr Pro Asn Gln Phe Glu Ala
299             145            150            155            160
301 Glu Leu Leu Thr Gly Phe Arg Ile Gln Ser Glu Gly His Gly Arg Glu
302             165            170            175
W--> 304 Ala Xaa Arg Leu Leu His Ala Ala Gly Pro Ser Lys Xaa Ile Ile Thr
305             180            185            190
307 Ser Ile Asn Ile
308             195

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310 <210> SEQ ID NO: 7
311 <211> LENGTH: 773
312 <212> TYPE: DNA
313 <213> ORGANISM: Triticum aestivum
315 <400> SEQUENCE: 7
316 atggcgcggc cgccgacccct atccgtcgcg ctgccgtctg acaccggccg tgtgctcagc 60
317 atccagtccc acaccgtcca ggggtatggt ggcaacaaat cggccgtctt tcccctgcag 120
318 ctcccttggt ttgatgtgga tccaataaac tctgtacagt tttctaatac tacaggatac 180
319 ccaacattta gagggtcagt tcttaatggc aaacagctct gggaacttat tgaaggactg 240
320 gaggaataat agctgcttca ttatacccat ttattaacag gttatatagg ctgagtttcc 300
321 ttttttagata ctgtgctaca agttgttgag aaattgcgat cagttaatcc tgatcttgta 360
322 tatgtttgtg acccagttct aggtgatgaa ggaaaactat atgttcctca ggagctaata 420

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/081,301

DATE: 03/07/2002

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Input Set : N:\Crf3\RULE60\10081301.txt

Output Set: N:\CRF3\03072002\J081301.raw

L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:141 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3  
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:174 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:177 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4  
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:251 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:251 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:253 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:254 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:304 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:395 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9  
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:422 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10  
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:570 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:571 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:572 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:573 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:574 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:575 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:576 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:604 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:607 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12